

Figure 1A

1 CCACGCGTCCGAACATGGGCTGAGAGCCCCCAAGAGCATCTCTAAGACCGGAGTGGGC 60
 61 AGGGACCCGGGCTCTGAGGGGCTCAGGCTCCAGGCCGAAACTGCACGCGGTGCTGGCG 120
 121 TCAGGCCCGAGGCCAGCTACGCCTCCACGGCTCCCTAATCGCCATTTCGGGGCTTGCG 180
 181 GGAGCACCTGGGAGGCTCCACCCGAGCCAGACACTGCCTGCCCCACGCCCCCTCCAGGA 240
 241 CCCTCGAAGGAGAAGGAAATCGGGACTGGCCCAGCGTCCCGTGCTCTAGAAGGCGGGCTA 300
 301 CTGCCCCGTCCCAAGCAGGGGAGGAGGACGAGCGAGGGCGTCACTCATTCTGTCCCCCGC 360
 361 GGAAGGATGAGGAAGCTCTGTTTACCTAAATGAAAAGCTTTCTAGGAGGAAGTCCTAAGT 420
 421 GAACAATGATGCATGAGGATGCAATCTTACAGACACAGGGGTCTCCCTATGTTGTTCAAG 480
 481 CTGGTCTCGAACTCCTGGCCTCAAGTGATCCTCCTGCCTCGACCTCTCAAAGCTCTGGTA 540
 541 TTATAGGCAAGGAGCCCAGTGATAACAAATGGCTGTAGATGCTTTTCCTCCATCAAGCTT 600
 601 CCAGGAGGAGATGAGATGGAGCCCCATCGCTGAGCCAAGAATTCTAATTTTCATCCCTTTGG 660
 661 TCTTTGTTTCATGCTGTGTTCTGCCTGGAATATTCTCCATCTTCTTTGCCTGGAAAAGTAT 720
 721 TACTTACTGAAACCTTGAAGCCACTACCTTCTCTAAACATTGACAATGCATAACCATTTG 780
 781 CCGAGCGTTCTTCCCCGACTGCATCCGTTTAGTCTACTGAGAGGCAGCTCAGCGTTCCC 840
 841 AAGGAGACAGATGTCTAGCTTTGCTCTTTCTGTCTGTGTGATGCTGGAGAATCGATATGC 900
 901 CCCTGGGCCTCCATCTCCATCTGTAAAACAAGGCATCAGATACCCACCTGGTGGCCCCG 960
 961 TCCTCACTTGGGAACCAAGTCAACATGCCTTCTGGAAGTCTCTCTTGTCACTCCAAGAAAA 1020
 1021 GATCCCCAGGAAACCTACAGGGACTATGTCCGCAGGAAATTCCGGCTCATGGAAGACCGC 1080
 1081 AATGCGCGCCTAGGGGAATGTGTCAACCTCAGCCACCGGTACACCCGGCTCCTGCTGGTG 1140
 1141 AAGGAGCACTCAAACCCCATGCAGGTCCAGCAGCAGCTTCTGGACACAGGCCGGGGACAC 1200

Figure 1B

1201 GCGAGGACCGTGGGACACCAGGCTAGCCCCATCAAGATAGAGACCCCTCTTTGAGCCAGAC 1260

1261 GAGGAGCGCCCCGAGCCACCGCGCACCGTGGTCATGCAAGGCGCGGCAGGGATAGGGAGA 1320
1 M

1321 TGAACCAGAGTGCCACGGAATGCAGCATGCAAGACCTCATCTTCAGCTGCTGGCCTGAGC 1380
2 N Q S A T E C S M Q D I F S C W P E P 21

1381 CCAGCGCGCCTCTCCAGGAGCTCATCCGAGTTCCCGAGCGCCTCCTTTTCATCATCGACG 1440
22 S A P L Q E L I R V P E R L F I I D G 41

1441 GCTTCGATGAGCTCAAGCCTTCTTCCACGATCCTCAGGACCCCTGGTGCCTCTGCTGGG 1500
42 F D E L K P S F H D P Q G P W C L C W E 61

1501 AGGAGAAACGCCCCACGGAGCTGCTTCTTAACAGCTTAATTCGGAAGAAGCTGCTCCCTG 1560
62 E K R P T E L N S I R K K L P E 81

1561 AGCTATCTTTGCTCATCACCACACGGCCCCACGGCTTTGGAGAAGCTCCACCGTCTGCTGG 1620
82 L S L I T T R P T A L E K L H R L E 101

1621 AGCACCCACGGCATGTGGAGATCCTGGGCTTCTCTGAGGCAGAAAGGAAGGAATACTTCT 1680
102 H P R H V E I L G F S E A E R K E Y F Y 121

1681 ACAAGTATTTCCACAATGCAGAGCAGGCGGGCCCAAGTCTTCAATTACGTGAGGGACAACG 1740
122 K Y F H N A E Q A G Q V F N Y V R D N E 141

1741 AGCCTCTCTTACCATGTGCTTCGTCCTCCCTTGGTGTGCTGGGTGGTGTGTACCTGCCTCC 1800
142 P L F T M C F V P L V C W V V C T C L Q 161

1801 AGCAGCAGCTGGAGGGTGGGGGGCTGTTGAGACAGACGTCCAGGACCACCACTGCAGTGT 1860
162 Q Q L E G G G L L R Q T S R T T T A V Y 181

1861 ACATGCTCTACCTGCTGAGTCTGATGCAACCCAAGCCGGGGGGGGCGCCTCCAGCCCC 1920
182 M L Y L L S L M Q P K P G A P R L Q P P 201

1921 CACCCAACCAGAGAGGGTTGTGCTCCTTGGCGGCAGATGGGCTCTGGAATCAGAAAATCC 1980
202 P N Q R G C S L A A D G L W N Q K I L 221

1981 TATTTGAGGAGCAGGACCTCCGGAAGCACGGCCTAGACGGGGAAGACGTCTCTGCCTTCC 2040
222 F E E Q D L R K H G D G E D V S A F L 241

2041 TCAACATGAACATCTTCCAGAAGGACATCAACTGTGAGAGGAGCTTCTTGCACTCACCA 2100
242 N M N I F Q K D I N C E R S F L A L T S 261

Figure 1C

2101 GCCGCTTCCTGTTTGGACTCCTGAACGAGGAGACCAGGAGCCACCTGGAGAAGAGTCTCT 2160
 262 R F F G L L N E E T R S H L E K S L C 281
 2161 GCTGGAAGGTCTCGCCGACATCAAGATGGACCTGTTGCAGTGGATCCAAAGCAAAGCTC 2220
 282 W K V S P H I K M D L L Q W I Q S K A Q 301
 2221 AGAGCGACGGCTCCACCCTGCAGCAGGGCTCCTTGGAGTTCTTCAGCTGCTTGTACGAGA 2280
 302 S D G S T L Q Q G S L E F F S L Y E I 321
 2281 TCCAGGAGGAGGAGTTTATCCAGCAGGCCCTGAGCCACTTCCAGGTGATCGTGGTCAGCA 2340
 322 Q E E E F I Q Q A L S H F Q V I V V S N 341
 2341 ACATTGCCTCCAAGATGGAGCACATGGTCTCCTCGTTCTGTCTGAAGCGCTGCAGGAGCG 2400
 342 I A S K M E H M V S S F C L K R C R S A 361
 2401 CCCAGGTGCTGCACCTGTATGGCGCCACCTACAGCGCGGACGGGGAAGACCGCGCGAGGT 2460
 362 Q V H H Y G A T Y S A D G E D R A R C 381
 2461 GCTCCGCGAGGAGCGCACACGCTGTTGGTGCAGCTACCAGAGAGGACCGTTCTGCTGGACG 2520
 382 S A G A H T L L V Q L P E R T V L L D A 401
 2521 CCTACAGTGAACATCTGGCAGCGGCCCTGTGCACCAATCCAAACCTGATAGAGCTGTCTC 2580
 402 Y S E H A A A L C T N P N L I E S L 421
 2581 TGTACCGAAATGCCCTGGGCAGCCGGGGGTGAAGCTGCTCTGTCAAGGACTCAGACACC 2640
 422 Y R N A L G S R G V K L L C Q G L R H P 441
 2641 CCAACTGCAAACCTCAGAACCTGAGGTAAATTTATCATATATAACATGATATTTTGAA 2700
 442 N C K L Q N L R * 449
 2701 TAAATATATTGGCCAGGTATGATGGCTCACGCCTGTAATTCAGCACTTTGGGAGGCCCA 2760
 2761 GATGGGGAGGATCACTTGACCCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCC 2820
 2821 CATCTCTACTAAAAATACCAAAATGAGCCAGGCATGGTGGCACACGTCTGTAAGCCCAGC 2880
 2881 TACTCAGGAGGCCAAGGCAGGAGGATTGCTTCAACCCAGGAGGCAGAGTTGTGGCTGAA 2940
 2941 GAGGTGCCGCATCTCCAGCTCAGCCTGCGAGGACCTCTCTGCAGCTCTCATAGCCAATAA 3000
 3001 GAATTTGACAAGGATGGATCTCAGTGGCAACGGCGTTGGATTCCCAGGCATGATGCTGCT 3060
 3061 TTGCGAGGGCCTGCGGCATCCCCAATGCAGGCTGCAGATGATTGAGGAAGTGTCA 3120

Figure 1D

3121 GCTGGAGTCCGGGGCTTGTCTCAGGAGATGGCTTCTGTGCTTGGCACCAACCCACATCTGGT 3180
 3181 TGAGTTGGACCTGACAGGAAATGCACTGGAGGATTGGGCTGAGGTTACTATGCCAGGG 3240
 3241 ACTGAGGCACCCAGTCTGCAGACTACGGACTTTGTGGCTGAAGATCTGCCGCCTCACTGC 3300
 3301 TGCTGCCTGTGACGAGCTGGCCTCAACTCTCAGTGTGAACCAGAGCCTGAGAGAGCTGGA 3360
 3361 CCTGAGCCTGAATGAGCTGGGGGACCTCGGGGTGCTGCTGCTGTGTGAGGGCCTCAGGCA 3420
 3421 TCCCACGTGCAAGCTCCAGACCCTGCGGTGAGTCCCGTTTGTCTCACCACGCTAGGAGTC 3480
 3481 CCAATCCATGAACGCAGCCCTCTCACCTGGGACCACGGAGGCCAGGTTGTCTCTGCTCCT 3540
 3541 AAACCTCTAGCTACTACATCAGCCCTTTTTTTTTTTTTTTTGGAGACTCCCAAGTAGCTGAG 3600
 3601 ATTACAGGCGCCCGCCACCAAGCCAGCTAATTTTTTGTATTTTAGTAGAGACAGGGTT 3660
 3661 TCATCATGTTAGCAGGATGGTCTCGATCTACTGACCTCATGATCTGCCTGCCTTGGCCTC 3720
 3721 CCAAAGTGCTGGGATTACAGGCTTGAGCCACTGCACCCAGCCTACATCAGCCTTTTAA 3780
 3781 AGGATTTTTCTGGCCGGGCATGGTGGCTGACACCTTAATCCAGCACTTTTGGGAGGCCG 3840
 3841 AGGTGGGAGGATCACCTGAGGTGGGAATTCGAGACCAGCCTGACCAACATGTAGAAACA 3900
 3901 CCCCATCTGTACTAAAAATACAAAAGTAGCCAGGCATGGTGGTGCATGCCTATAATGCCA 3960
 3961 GCTACTCGCGAGGCTGAGGCAGGAGAATCCGTTGAACCCGGGAGGTGGAAGTTGCTGTGA 4020
 4021 GCTGAGATGGAGCCATTGCACTCCAGTCTGGGCAACAAGAGCGAAACTCCGTCTCAAAA 4080
 4081 AAAAAAGGGGGGGTCTTCTGACGCACGGCCCTTGCACAAGCAATTCTTATCCCTGG 4140
 4141 CATGCCTTCTGCTCTCTGTCCCCTCTTGCCTGGAGAAGTTCAATTTTCTTCTGAACAC 4200
 4201 TCTTTACTTTGTATTTTGGAGACAGGGTCTTGTCTGTCAACAGTGTGAGTGGAGTGGT 4260
 4261 GTGATCATAGCCCCGACATCCTGGGCTGAAGCCATCCTCCCAACTCAGCCTCCTGAGTAGC 4320

Figure 1E

4321 TGGGACTGCAAGCGCATGCCACCACAGATGGCTAATTTTACTTTTTTTTGGAGATTTTG 4380
4381 CCACTGCACTCCAGCCTGGATGACAGAGCGAGATTCATCTCAAAAAAAAAAAGAAAAA 4440
4441 TTTGTAATTTGTGTATATGTGTGTGTGGTGGCATTCACAAGCATAGGAGCTATGCCAAC 4500
4501 TGTATCTCCTAGTGACTAGTATAAGACGTGGGTAGAAGTGCTCAAAAAACACACTTTGTG 4560
4561 TATTTTTTTTATCAAGGCACCAGCAAAAAACAAAAACAAAAATCACACACGCGGCTGG 4620
4621 GCGCGGTGGCTCATGCCTGTAAACCCAGCACTTTGGGAGGCTGAGGCGGGTGGATCACGA 4680
4681 GGTCAAGAGATGGAGACCATCCTGGCCAACGGTGAAACCCCGTCTCTACTAAAAATACA 4740
4741 AAAATTAGCTGGGCGTGGTGGTGTGCACCTGTAGTCACAGCTACTCAGGAGGCTGAGGCA 4800
4801 GAAGAATCACTTGAACCCAGGAGGCGGAGGTTGCAGTGAGCCGAGATCGCGCCACTGCAC 4860
4861 TCCAGCCTGGGCGACAGAGTGGGACTCCATCTCAAAAAAAAAAAAAAAAAAAAAAAAAAA 4920
4921 AAAAAAAAAA 4931

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Figure 2A

		1	50
HNTTBMyl	(1)	-----	-----
caspase_recruitment_protein	(1)	MAAGAWGRILACYLEFLKKEELKEFOLHANKAHSRSSSGETPAQPEKTS	SG
cryopyrin	(1)	-MASTRCKLARYLEDLEVLKFKMHLEDFYFOKGCPLPFRCTEKALH	
NOD1	(1)	-----MEEQCHSEMEKPSSESHPHIQLKSNR--ELLVH	
		51	100
HNTTBMyl	(1)	-----	-----
caspase_recruitment_protein	(51)	MEVPSYLVACYGEORAWDLALHTWEOMGLRSLCAQAOEGAGHSFPYSP	
cryopyrin	(50)	UDEALMLIDFNCEKAWAMAWIFAAINRRDIYEKAKRDEPKWGSNARV	
NOD1	(34)	IRNTQCLVDN-----LLKNDYFSAEDARIVACPTQPKVRKILDVQ	
		101	150
HNTTBMyl	(1)	-----	-----
caspase_recruitment_protein	(101)	SEPHLGSPSQPTSTAVLMPWTHLPACCTGSESRVIRQIDTSGPGRRE	
cryopyrin	(100)	SN-----PIVICQDSTEEEMGLILEYLRISICKMKKDYRKVK	
NOD1	(77)	SK-----GEF--VSEFFVYLLOQADAYMDLRFWLLLEIGSP	
		151	200
HNTTBMyl	(1)	-----	-----
caspase_recruitment_protein	(151)	ISASHLYQAPPSSEDHESPSQESPNAPTSTAVLGSWGSPQPSLAPREQE	
cryopyrin	(141)	YVRSRFQCEDRNARLG-----	
NOD1	(112)	SILTQSKVMNTLEVSRYTCLR-----	
		201	250
HNTTBMyl	(1)	-----	-----
caspase_recruitment_protein	(201)	APGTQWPLDETSGIYYTEIREREREKSEKGRPPWAAVVGTPPOAHSSLOP	
cryopyrin	(158)	-----	-----
NOD1	(135)	-----	-----
		251	300
HNTTBMyl	(1)	-----MPKNSKTOREH	
caspase_recruitment_protein	(251)	HHHPWEPSVRESLCSTWPWKNEFDNOKFTQLLLQPHPRSQ--DPLVKRS	
cryopyrin	(158)	-----ESSLNKRYTRRLKEHRSQOEREQDLAI	
NOD1	(135)	-----HHGRDSKFLCYAQKELELEIYMDIME	
		301	350
HNTTBMyl	(13)	SSEHVIESVALLALEEPVDYKQSLNVAG-----EAG-GKQKAVSE	
caspase_recruitment_protein	(300)	WPDVVEENRCHLEIDRLLEGLDQMER--IVTQGAAGICKSTLARV	
cryopyrin	(189)	GKTKICESPVSPFKMDLFDPDDEHSEPVH-TVTFQGAAGIGKILARKM	
NOD1	(166)	LVGHSNESGSLNSLACLIDHTTCLNEQGETFLGDCAGVGSNLLCAL	
		351	400
HNTTBMyl	(54)	ELTTEDRPANNKILOYLLAQIGFSVLEGNWR--EPYECCKNCGGAYLV	
caspase_recruitment_protein	(348)	KEAMRGCOLYDRFOHFPYFSCRELAOSKVVS--DRLIGKDGSTAPAE	
cryopyrin	(238)	MLDWAAGILYDRFYFYTHCREVSLVTQRS--LDDLIMSCCPDNEP	
NOD1	(216)	QSLNATGRIDAG-VKKEPFRCRMFSCKFESDRLOQDLDFKHICYPERD	
		401	450
HNTTBMyl	(101)	EYLVELITIGIFLFFLELAVGQIRRCSTGVVHYICPRLGGIGFSSCIVC	
caspase_recruitment_protein	(395)	---TROITSEPRLEFLDGVDEPGWVLEPSSSELCHMSQ--PPADAL	
cryopyrin	(285)	---THKIYRKESRLFLTDGDELOQADDEHIGPLCDWQK-AERCDL	
NOD1	(265)	EEVFAFLRFPHVALFTEDGDELHSLDLSRVEDSSCPWE-PAHPLVT	
		451	500
HNTTBMyl	(151)	LFVGLYYNLTIGWSTFYFFKSFQYPLWSECPVVRNGSVAVVEACCKES	
caspase_recruitment_protein	(440)	LSLICKLLEPASELITARTALQNLPSLEQARWVEVLGFSESSRKEY	
cryopyrin	(330)	LSLIRKKLLPEASLITIREVALEKIQHLLHPRHVELGFSERKEY	
NOD1	(314)	LALLISGKLLKASKLEARTGIEVPROFLR--KKVLRGFSPSHLNAV	
		501	550
HNTTBMyl	(201)	ATTYVWYREALDSDSSESGTNWNTLCLLVWSTVGMAYVVGIS-	
caspase_recruitment_protein	(490)	FYRYTDEROATRAFRVSNKELWALCLVFWVWMACTCLVQOMKRKE-	
cryopyrin	(380)	FEKYFEDPAQARAASLQENEVLTMCPLVCWLTCTGLQOMESCK-	
NOD1	(361)	ARRMFEERALQDRLLSQEANPNLCASVPLFCWLTFRCEQFRAAFEG	
		551	600
HNTTBMyl	(250)	---GVMYFSSIFPVVLAELVRC-----LLLRGAV	
caspase_recruitment_protein	(539)	--KTLTSTKTTTLCLNYLAQALQAP-----LGPQL	
cryopyrin	(429)	--SPAQTSKTTTAVVVFSSLLQPRGGS-----QBFGLCAHL	
NOD1	(411)	SPQIPDCMTLTQVFLVTEVHLNRMQPSLVQRNTRSPVETILAGRITL	

[illegible][illegible]

[illegible][illegible]

Figure 3

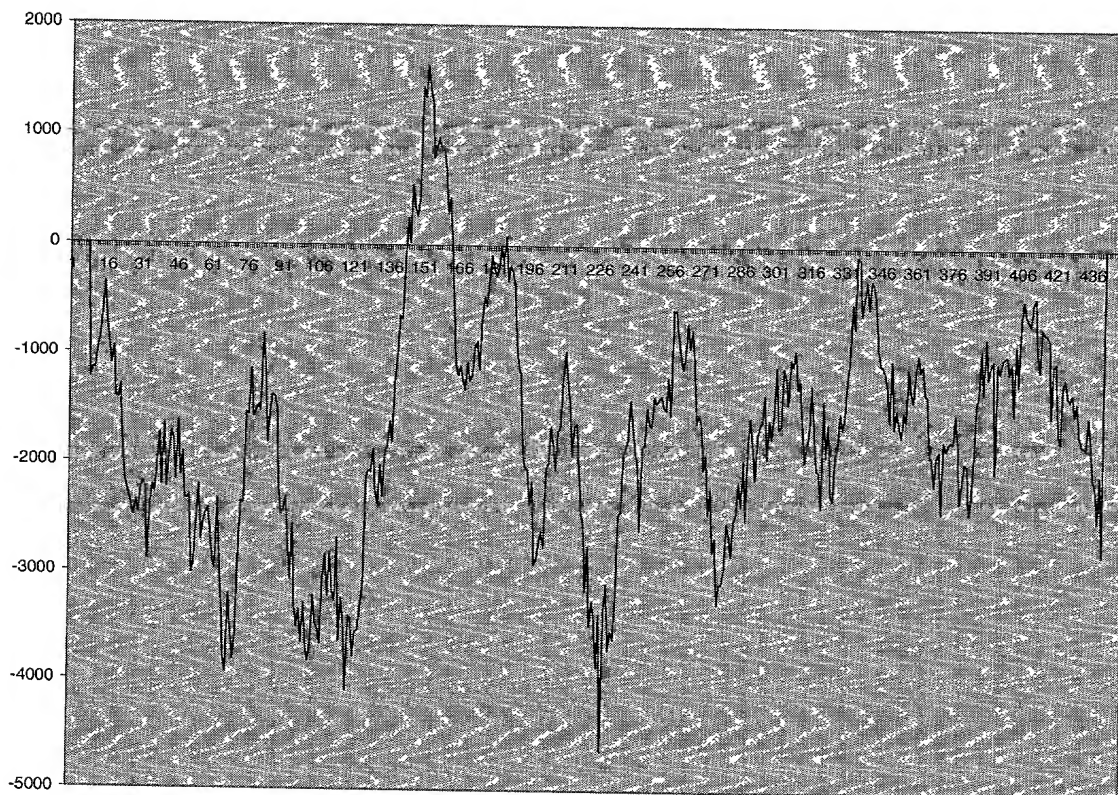


Figure 4

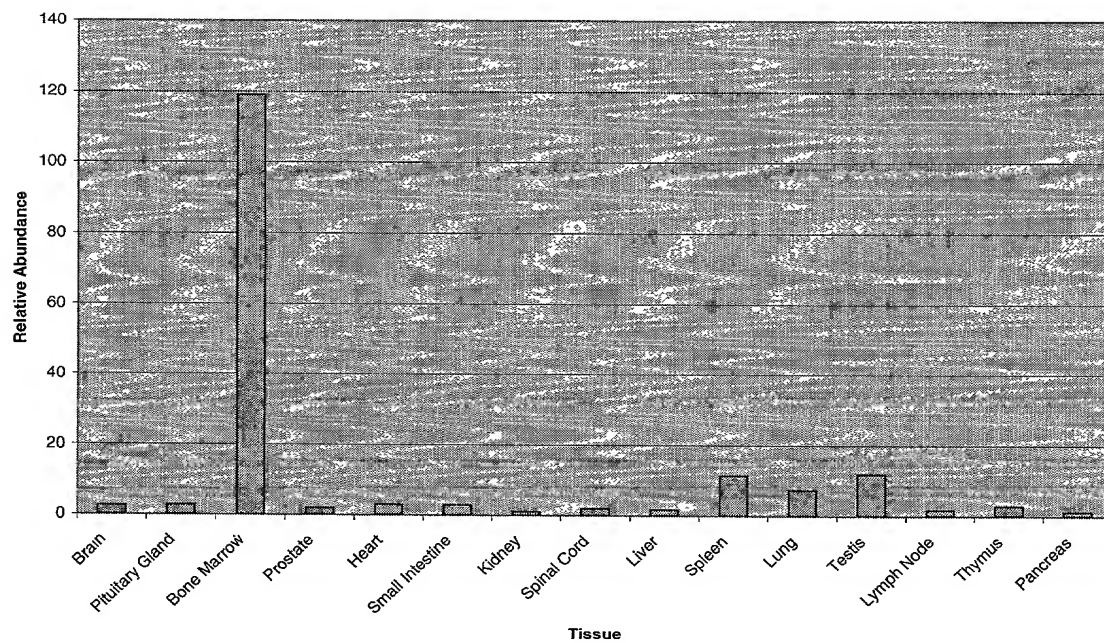


Figure 5.

<u>Protein</u>	<u>Genbank ID</u>	<u>Percent Identity</u>	<u>Percent Similarity</u>
human caspase recruitment protein 7	gil10198209	35%	48%
human NOD caspase recruitment protein 4	gil5174617	25%	38%
human cryopyrin protein	gil17027237	51.7%	64.0%